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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/919,932

DATE: 11/26/2001
 TIME: 15:01:27

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3 <110> APPLICANT: MOECKEL, BETTINA
 4 PFEFFERLE, WALTER
 5 HUTHMACHER, KLAUS
 6 RUECKERT, CHRISTIAN
 7 KALINOWSKI, JOERN
 8 PUEHLER, ALFRED
 9 BINDER, MICHAEL
 10 GREISSINGER, DIETER
 11 THIERBACH, GEORG
 13 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METY GENE
 15 <130> FILE REFERENCE: 211707US0X
 17 <140> CURRENT APPLICATION NUMBER: 09/919,932
 18 <141> CURRENT FILING DATE: 2001-08-02
 20 <150> PRIOR APPLICATION NUMBER: DE 10043334.0
 21 <151> PRIOR FILING DATE: 2000-09-02
 23 <150> PRIOR APPLICATION NUMBER: DE 10109690.9
 24 <151> PRIOR FILING DATE: 2001-02-28
 26 <150> PRIOR APPLICATION NUMBER: US 60/294,252
 27 <151> PRIOR FILING DATE: 2001-05-31
 29 <160> NUMBER OF SEQ ID NOS: 2
 31 <170> SOFTWARE: PatentIn version 3.1
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 1720
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Corynebacterium glutamicum
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
 40 <222> LOCATION: (200)..(1510)
 41 <223> OTHER INFORMATION:
 44 <400> SEQUENCE: 1
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 49 gtcttattgc atagaccaaag ctgttcagta qgggtgcattgg gagaagaatt tcctaataaa 180
 51 aactcttaag gacctccaa atg cca aag tac gac aat tcc aat gct gac cag 232
 52 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln
 53 1 5 10
 55 tgg ggc ttt gaa acc cgc tcc att cac gca ggc cag tca gta gac gca 280
 56 Trp Gly Phe Glu Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala
 57 15 20 25
 59 cag acc agc gca cga aac ctt ccg atc tac caa tcc acc gct ttc gtg 328
 60 Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val
 61 30 35 40
 63 ttc gac tcc gct gag cac gcc aag cag cgt ttc gca ctt gag gat cta 376
 64 Phe Asp Ser Ala Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu
 65 45 50 55
 67 ggc cct gtt tac tcc cgc ctc acc aac cca acc gtt gag gct ttg gaa 424
 68 Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu

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71	aac	cgc	atc	gct	tcc	ctc	gaa	ggg	ggc	gtc	cac	gct	gta	gcg	ttc	tcc	472	
72	Asn	Arg	Ile	Ala	Ser	Leu	Glu	Gly	Gly	Val	His	Ala	Val	Ala	Phe	Ser		
73																	90	
75	tcc	gga	cag	gcc	gca	acc	acc	acc	gcc	att	ttg	aac	ctg	gca	gga	gcf	520	
76	Ser	Gly	Gln	Ala	Ala	Thr	Thr	Asn	Ala	Ile	Leu	Asn	Leu	Ala	Gly	Ala		
77																	105	
79	ggc	gac	cac	atc	gtc	acc	tcc	cca	ccg	ctc	tac	ggg	ggc	acc	gag	act	568	
80	Gly	Asp	His	Ile	Val	Thr	Ser	Pro	Arg	Leu	Tyr	Gly	Gly	Thr	Glu	Thr		
81																	120	
83	cta	tcc	ctt	act	act	ttc	aat	ccg	ctg	ggg	atc	gtt	gtt	tcc	tcc	gtg	616	
84	Leu	Phe	Leu	Ile	Thr	Leu	Asn	Arg	Leu	Gly	Ile	Asp	Val	Ser	Phe	Val		
85																		
87	gaa	aac	ccc	gac	gac	cct	gag	tcc	tgg	cag	gca	gcc	gtt	cag	cca	aac	664	
88	Glu	Asn	Pro	Asp	Asp	Pro	Glu	Ser	Ser	Trp	Gln	Ala	Ala	Val	Gln	Pro	Asn	
89																	155	
91	acc	aaa	gca	tcc	tcc	ggc	gac	ggg	act	ttc	gcc	aac	cca	cag	gca	gac	gtc	712
92	Thr	Lys	Ala	Phe	Phe	Gly	Glu	Thr	Phe	Ala	Asn	Pro	Gln	Ala	Asp	Val		
93																	170	
95	ctg	gat	att	cct	ggc	gtg	gtc	gaa	gtt	gcg	cac	ccg	aac	agc	gtt	cca	760	
96	Leu	Asp	Ile	Pro	Ala	Val	Ala	Glu	Val	Ala	His	Arg	Asn	Ser	Val	Pro		
97																	185	
99	ctg	atc	atc	gac	aac	acc	acc	atc	gtt	acc	gca	gcg	ctc	gtg	ccg	ccg	808	
100	Leu	Ile	Ile	Asp	Asn	Thr	Ile	Ala	Thr	Ala	Ala	Leu	Val	Arg	Pro	Leu		
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103	gag	ctc	ggc	gca	gac	gtt	gtc	gtc	gtc	gct	tcc	ctc	acc	aag	ttc	tac	acc	856
104	Glu	Leu	Gly	Ala	Asp	Val	Val	Val	Val	Ala	Ser	Leu	Thr	Lys	Phe	Tyr	Thr	
105																	215	
107	ggc	aac	ggc	tcc	gga	ctg	ggc	ggc	gtg	ctt	atc	gac	ggc	gga	aag	ttc	904	
108	Gly	Asn	Gly	Ser	Gly	Leu	Gly	Gly	Val	Leu	Asp	Gly	Gly	Lys	Phe			
109																	235	
111	gat	tgg	act	gtc	gaa	aag	gat	gga	aag	cca	gtt	ttc	ccc	tac	ttc	gtc	952	
112	Asp	Trp	Thr	Val	Gly	Lys	Asp	Gly	Lys	Pro	Val	Phe	Pro	Tyr	Phe	Val		
113																	250	
115	act	cca	gat	gtt	gtc	gtt	tac	cac	gga	ttg	aag	tac	qca	gac	ctt	ggf	1000	
116	Thr	Pro	Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala		
117																	265	
119	cca	gcc	tcc	ggc	ctc	aag	gtt	ccg	gtt	ggc	ctt	ctt	cca	ccg	gac	acc	1048	
120	Pro	Ala	Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly		
121																	280	
123	tcc	acc	ctc	tcc	gca	ttc	aac	gca	tgg	gtt	gca	gtc	cag	ggc	atc	gac	1096	
124	Ser	Thr	Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp		
125																	295	
127	acc	ctt	tcc	ctg	ccg	ctg	gag	ccg	cac	aac	gaa	aac	gcc	atc	aag	gtt	1144	
128	Thr	Leu	Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	Glu	Asn	Ala	Ile	Lys	Val		
129																	315	
131	gca	gaa	ttc	ctc	aac	aac	cac	gag	aag	gtg	gaa	aag	gtt	aac	ttc	gca	1192	
132	Ala	Glu	Phe	Leu	Asn	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala		
133																	330	

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136 Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu	
137 335 340 345	
139 aag tac acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat	1288
140 Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp	
141 350 355 360	
143 gag gct tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca	1336
144 Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala	
145 365 370 375	
147 aac atc ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc	1384
148 Asn Ile Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr	
149 380 385 390 395	
151 cat tca cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag	1432
152 His Ser Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Gln	
153 400 405 410	
155 tcc acc gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc	1480
156 Ser Thr Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile	
157 415 420 425	
159 gct gac ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc	1530
160 Ala Asp Leu Glu Gly Phe Ala Ala Ile	
161 430 435	
163 tcacccgaa aacgcgttggg tttttcttt tcgactcggt gagaatgcaa actagactag	1590
165 acagacgtgt ccatatacac tggacgaatgtttatgtcttg tccacccaga acacggcggtt	1650
167 attttcatgc ccacccctcgc gccttcaggta caacttgaaa tccaaagcgat cggtgtatgtc	1710
169 tcacccgaaag	1720
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174 <212> TYPE: PRT	
175 <213> ORGANISM: Corynebacterium glutamicum	
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187 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu	
188 35 40 45	
191 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser	
192 50 55 60	
195 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser	
196 65 70 75 80	
199 Leu Glu Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala	
200 85 90 95	
203 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val	
204 100 105 110	
207 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr	
208 115 120 125	
211 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp	
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223	Val	Ala	Glu	Val	Ala	His	Arg	Asn	Ser	Val	Pro	Leu	Ile	Ile	Asp	Asn
224																190
227	Thr	Ile	Ala	Thr	Ala	Ala	Leu	Val	Arg	Pro	Leu	Glu	Leu	Gly	Ala	Asp
228																205
231	Val	Val	Val	Ala	Ser	Leu	Thr	Lys	Phe	Tyr	Thr	Gly	Asn	Gly	Ser	Gly
232																220
235	Leu	Gly	Gly	Val	Leu	Ile	Asp	Gly	Gly	Lys	Phe	Asp	Trp	Thr	Val	Glu
236	225															240
239	Lys	Asp	Gly	Lys	Pro	Val	Phe	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala
240																255
243	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu
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247	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala
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251	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg
252																300
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256	305															320
259	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser
260																335
263	Pro	Trp	Tyr	Ala	Thr	Lys	Glu	Lys	Leu	Gly	Leu	Lys	Tyr	Thr	Gly	Ser
264																350
267	Val	Leu	Thr	Phe	Glu	Ile	Lys	Gly	Gly	Lys	Asp	Glu	Ala	Trp	Ala	Phe
268																365
271	Ile	Asp	Ala	Leu	Lys	Leu	His	Ser	Asn	Leu	Ala	Asn	Ile	Gly	Asp	Val
272																380
275	Arg	Ser	Leu	Val	Val	His	Pro	Ala	Thr	Thr	Thr	His	Ser	Gln	Ser	Asp
276	385															400
279	Glu	Ala	Gly	Leu	Ala	Arg	Ala	Gly	Val	Thr	Gln	Ser	Thr	Val	Arg	Leu
280																415
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287	Gly	Phe	Ala	Ala	Ile											
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